

SEQUENCE LISTING

<110> Suntory Limited

<120> MARCHANTIALES-DERIVED UNSATURATED FATTY ACID SYNTHETASE GENES
AND USE OF THE SAME

<130>

<150> JP 2003-425673

<151> 2003-12-22

<160> 46

<170> PatentIn Ver. 2.1

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<211> 2519

<212> DNA

<213> Marchantia polymorpha

<220>

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<222> (253)..(1698)

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Ser Arg Lys Glu Gln Gln Gln Gln Gln Ser Ser Pro Glu Ala

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Ser Thr Pro Ala Ala Gln Gln Glu Lys Ser Ile Ser Arg Glu Ser Ile

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Pro Glu Gly Phe Leu Thr Val Glu Glu Val Ser Lys His Asp Asn Pro
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Ser Asp Cys Trp Ile Val Ile Asn Asp Lys Val Tyr Asp Val Ser Ala
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Phe Gly Lys Thr His Pro Gly Gly Pro Val Ile Phe Thr Gln Ala Gly
95 100 105

cgc gac gcc acg gat tct ttc aag gtt ttc cac tcc gcc aag gcg tgg 627
Arg Asp Ala Thr Asp Ser Phe Lys Val Phe His Ser Ala Lys Ala Trp
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145 150 155

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Arg Ser Gln Leu Phe Lys Ser Ser Lys Met Tyr Tyr Val Thr Lys Cys
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Val Thr Asn Phe Ala Ile Leu Ala Ala Ser Leu Ala Val Ile Ala Trp
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Val Thr Glu Asn Arg Ser Leu Asn Thr Tyr Phe Gly Gly Leu Phe Trp
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Gly Asn Phe Ala Gln Gly Tyr Ser Val Gly Trp Trp Lys Thr Lys His
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Asn Val His His Ala Ala Thr Asn Glu Cys Asp Asp Lys Tyr Gln Pro
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Ile Asp Pro Asp Ile Asp Thr Val Pro Leu Leu Ala Trp Ser Lys Glu
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Ile Leu Ala Thr Val Asp Asp Gln Phe Phe Arg Ser Ile Ile Ser Val
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Leu His Ser Ser Trp Ala His Ala Ser Asn Phe Glu Met Pro Arg Tyr
320 325 330

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Met Arg Trp Ala Glu Lys Ala Ser Leu Leu Gly His Tyr Gly Ala Ser
335 340 345

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Ile Gly Ala Ala Phe Tyr Ile Leu Pro Ile Pro Gln Ala Ile Cys Trp
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Asn Asp Trp Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu
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Phe Pro Ser Leu Pro Arg His Asn Leu Ala Lys Val Ala Pro His Val
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Lys Ala Leu Cys Ala Lys His Tyr Glu Glu Leu Ser Leu
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Gly Thr Gly Val Cys Arg Val Phe Asn Arg Leu Val Glu Val Ala Tyr
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Ala Ala Lys Val
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Ala Ala Gln Gln Glu Lys Ser Ile Ser Arg Glu Ser Ile Pro Glu Gly
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 Phe Leu Thr Val Glu Glu Val Ser Lys His Asp Asn Pro Ser Asp Cys
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 Thr His Pro Gly Gly Pro Val Ile Phe Thr Gln Ala Gly Arg Asp Ala
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 Thr Asp Ser Phe Lys Val Phe His Ser Ala Lys Ala Trp Gln Phe Leu
 115 120 125
 Gln Asp Leu Tyr Ile Gly Asp Leu Tyr Asn Ala Glu Pro Val Ser Glu
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 Leu Phe Lys Ser Ser Lys Met Tyr Tyr Val Thr Lys Cys Val Thr Asn
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 Tyr Leu Ala Val Leu Cys Ser Ser Phe Leu Leu Ala Leu Phe Trp Gln
 195 200 205
 Gln Cys Gly Trp Leu Ser His Asp Phe Leu His His Gln Val Thr Glu
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 Asn Arg Ser Leu Asn Thr Tyr Phe Gly Gly Leu Phe Trp Gly Asn Phe
 225 230 235 240
 Ala Gln Gly Tyr Ser Val Gly Trp Trp Lys Thr Lys His Asn Val His
 245 250 255
 His Ala Ala Thr Asn Glu Cys Asp Asp Lys Tyr Gln Pro Ile Asp Pro
 260 265 270
 Asp Ile Asp Thr Val Pro Leu Leu Ala Trp Ser Lys Glu Ile Leu Ala
 275 280 285
 Thr Val Asp Asp Gln Phe Phe Arg Ser Ile Ile Ser Val Gln His Leu
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 Leu Phe Phe Pro Leu Leu Phe Leu Ala Arg Phe Ser Trp Leu His Ser
 305 310 315 320
 Ser Trp Ala His Ala Ser Asn Phe Glu Met Pro Arg Tyr Met Arg Trp
 325 330 335
 Ala Glu Lys Ala Ser Leu Leu Gly His Tyr Gly Ala Ser Ile Gly Ala
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 Ala Phe Tyr Ile Leu Pro Ile Pro Gln Ala Ile Cys Trp Leu Phe Leu
 355 360 365
 Ser Gln Leu Phe Cys Gly Ala Leu Leu Ser Ile Val Phe Val Ile Ser
 370 375 380
 His Asn Gly Met Asp Val Tyr Asn Asp Pro Arg Asp Phe Val Thr Ala
 385 390 395 400
 Gln Val Thr Ser Thr Arg Asn Ile Glu Gly Asn Phe Phe Asn Asp Trp
 405 410 415
 Phe Thr Gly Gly Leu Asn Arg Gln Ile Glu His His Leu Phe Pro Ser
 420 425 430
 Leu Pro Arg His Asn Leu Ala Lys Val Ala Pro His Val Lys Ala Leu
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cgaatccgcc gagagtgcat cgggattggg tagaaggagg agaaggagga gaagaggagg 180
aggaggagca gcg atg gag gcg tac gag atg gtg gat agt ttt gtg tcg 229
Met Glu Ala Tyr Glu Met Val Asp Ser Phe Val Ser
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Lys Thr Val Phe Glu Thr Leu Gln Arg Leu Arg Gly Gly Val Val Leu
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Thr Glu Ser Ala Ile Thr Lys Gly Leu Pro Cys Val Asp Ser Pro Thr
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ccg atc gtt ctt ggg ttg tgc tcc tac ttg aca ttc gtg ttt ctc ggg 373
Pro Ile Val Leu Gly Leu Ser Ser Tyr Leu Thr Phe Val Phe Leu Gly
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ctc att gtc atc aag agc ctg gat ctt aag ccc cgc tcc aag gag ccc 421
Leu Ile Val Ile Lys Ser Leu Asp Leu Lys Pro Arg Ser Lys Glu Pro
65 70 75

gcc att ttg aac ctg ttt gtg atc ttc cac aac ttc gtc tgc ttc gca 469
Ala Ile Leu Asn Leu Phe Val Ile Phe His Asn Phe Val Cys Phe Ala
80 85 90

ctc agt ctg tac atg tgc gtg gga att gtc cgt caa gct atc ctc aac 517
Leu Ser Leu Tyr Met Cys Val Gly Ile Val Arg Gln Ala Ile Leu Asn

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 Gly His Leu Leu Tyr Ile Phe Tyr Met Ser Lys Tyr Ile Glu Phe Met
 125 130 135 140

gac acg gtc att atg att ttg aag cgc aac acg cgc cag atc act gtg 661
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gcc tac cat gct cct ggc ggt gaa gct tat ttc tct gcc gca ttg aac 757
 Ala Tyr His Ala Pro Gly Gly Glu Ala Tyr Phe Ser Ala Ala Leu Asn
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tcc gga gta cat gtg ctc atg tac ctc tac tac ctt ttg gca gca act 805
 Ser Gly Val His Val Leu Met Tyr Leu Tyr Tyr Leu Leu Ala Ala Thr
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 Ala Tyr Tyr Asp Ile Lys Asn Asn Ser Pro Tyr Pro Gln Phe Leu Ile
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 Gln Ile Leu Phe Tyr Tyr Met Ile Ser Leu Leu Ala Leu Phe Gly Asn
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 270 275 280

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 Lys Ser Lys Lys Ala Glu
 285 290

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<213> Marchantia polymorpha

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35 40 45
Gly Leu Ser Ser Tyr Leu Thr Phe Val Phe Leu Gly Leu Ile Val Ile
50 55 60
Lys Ser Leu Asp Leu Lys Pro Arg Ser Lys Glu Pro Ala Ile Leu Asn
65 70 75 80
Leu Phe Val Ile Phe His Asn Phe Val Cys Phe Ala Leu Ser Leu Tyr
85 90 95
Met Cys Val Gly Ile Val Arg Gln Ala Ile Leu Asn Arg Tyr Ser Leu
100 105 110
Trp Gly Asn Ala Tyr Asn Pro Lys Glu Val Gln Met Gly His Leu Leu
115 120 125
Tyr Ile Phe Tyr Met Ser Lys Tyr Ile Glu Phe Met Asp Thr Val Ile
130 135 140
Met Ile Leu Lys Arg Asn Thr Arg Gln Ile Thr Val Leu His Val Tyr
145 150 155 160
His His Ala Ser Ile Ser Phe Ile Trp Trp Ile Ile Ala Tyr His Ala
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Pro Gly Gly Glu Ala Tyr Phe Ser Ala Ala Leu Asn Ser Gly Val His
180 185 190
Val Leu Met Tyr Leu Tyr Tyr Leu Leu Ala Ala Thr Leu Gly Lys Asn

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Leu Gln Met Phe Gln Phe Val Leu Asn Met Ile Gln Ala Tyr Tyr Asp		
225	230	235 240
Ile Lys Asn Asn Ser Pro Tyr Pro Gln Phe Leu Ile Gln Ile Leu Phe		
245	250	255
Tyr Tyr Met Ile Ser Leu Leu Ala Leu Phe Gly Asn Phe Tyr Val His		
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Lys Tyr Val Ser Ala Pro Ala Lys Pro Ala Lys Ile Lys Ser Lys Lys		
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Met Pro Pro His Ala Pro Asp Ser Thr Gly Leu Gly
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Pro Glu Val Phe Arg Leu Pro Asp Asp Ala Ile Pro Ala Gln Asp Arg
15 20 25

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Arg Ser Thr Gln Lys Lys Tyr Ser Leu Ser Asp Val Ser Lys His Asn
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Thr Pro Asn Asp Cys Trp Leu Val Ile Trp Gly Lys Val Tyr Asp Val
45 50 55 60

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Thr Ser Trp Val Lys Val His Pro Gly Gly Ser Leu Ile Phe Val Lys
65 70 75

gcg gga cag gat tca aca caa ctc ttt gat tct tat cac ccc ctc tat 650
Ala Gly Gln Asp Ser Thr Gln Leu Phe Asp Ser Tyr His Pro Leu Tyr
80 85 90

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Val Arg Lys Leu Leu Ala Gln Phe Cys Ile Gly Glu Leu Gln Thr Ser
95 100 105

gcg gga gat gag aag ttc aag tct tca acg ttg gag tat gct ggt gaa 746
Ala Gly Asp Glu Lys Phe Lys Ser Ser Thr Leu Glu Tyr Ala Gly Glu
110 115 120

gaa cat gaa gta ttt tac cac act ctc aag cag cgc gtg gaa acg tac 794
Glu His Glu Val Phe Tyr His Thr Leu Lys Gln Arg Val Glu Thr Tyr
125 130 135 140

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145 150 155

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Lys Ser Ala Val Ile Ile Gly Thr Leu Leu Cys Tyr Tyr Phe Gly
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175 180 185

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Met Gly Phe Cys Thr Ala Glu Val Gly Met Ser Ile Met His Asp Gly
190 195 200

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Ala Thr Leu Asp Leu Val Gly Ala Ser Ser Phe Met Trp Arg Gln Gln
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His Val Ala Gly His His Ser Phe Thr Asn Ile Asp His Tyr Asp Pro
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240 245 250

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Pro Arg Arg Trp Phe His Glu Tyr Gln His Ile Tyr Leu Gly Val Leu
270 275 280

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Tyr Gly Val Leu Ala Leu Lys Ser Val Leu Ile Asp Asp Phe Ser Ala
285 290 295 300

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Phe Phe Ser Gly Ala Ile Gly Pro Val Lys Ile Ala Gln Met Thr Pro
305 310 315

ctc gag atg ggc gtc ttc tgg gga ggg aag gtt gtg tac gca ctg tac 1370
Leu Glu Met Gly Val Phe Trp Gly Gly Lys Val Val Tyr Ala Leu Tyr
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Ile Gly Leu Tyr Ile Leu Ser Gln Leu Val Ala Gly Trp Thr Leu Ala
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Leu Phe Phe Gln Val Ala His Val Val Asp Asp Ala Val Phe Pro Val
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Ala Glu Thr Asp Gly Gly Lys Ala Lys Ile Pro Ser Gly Trp Ala Glu
385 390 395

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Met Gln Val Arg Thr Thr Asn Phe Ser Ser Arg Ser Met Phe Trp
400 405 410

aca cat att agt ggc ggt ctg aac cat cag atc gag cac cat ctt ttc 1658
Thr His Ile Ser Gly Gly Leu Asn His Gln Ile Glu His His Leu Phe
415 420 425

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Pro Gly Val Cys His Val His Tyr Pro Ser Ile Gln Pro Ile Val Lys
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Ala Thr Cys Asp Glu Phe Asn Val Pro Tyr Thr Ser Tyr Pro Thr Phe
445 450 455 460

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465 470 475

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Gln Asp Gly Leu Arg Leu Asp Gly
480 485

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<213> Marchantia polymorpha

<400> 6
Met Pro Pro His Ala Pro Asp Ser Thr Gly Leu Gly Pro Glu Val Phe
1 5 10 15
Arg Leu Pro Asp Asp Ala Ile Pro Ala Gln Asp Arg Arg Ser Thr Gln
20 25 30
Lys Lys Tyr Ser Leu Ser Asp Val Ser Lys His Asn Thr Pro Asn Asp
35 40 45
Cys Trp Leu Val Ile Trp Gly Lys Val Tyr Asp Val Thr Ser Trp Val
50 55 60
Lys Val His Pro Gly Gly Ser Leu Ile Phe Val Lys Ala Gly Gln Asp
65 70 75 80
Ser Thr Gln Leu Phe Asp Ser Tyr His Pro Leu Tyr Val Arg Lys Leu
85 90 95
Leu Ala Gln Phe Cys Ile Gly Glu Leu Gln Thr Ser Ala Gly Asp Glu
100 105 110
Lys Phe Lys Ser Ser Thr Leu Glu Tyr Ala Gly Glu Glu His Glu Val

115	120	125													
Phe	Tyr	His	Thr	Leu	Lys	Gln	Arg	Val	Glu	Thr	Tyr	Phe	Arg	Lys	Gln
130	135	140													
Lys	Ile	Asn	Pro	Arg	Tyr	His	Pro	Gln	Met	Leu	Val	Lys	Ser	Ala	Val
145	150	155	160												
Ile	Ile	Gly	Thr	Leu	Leu	Cys	Tyr	Tyr	Phe	Gly	Phe	Phe	Trp	Ser	
165	170	175													
Gln	Asn	Val	Leu	Leu	Ser	Met	Phe	Leu	Ala	Ser	Ile	Met	Gly	Phe	Cys
180	185	190													
Thr	Ala	Glu	Val	Gly	Met	Ser	Ile	Met	His	Asp	Gly	Asn	His	Gly	Ser
195	200	205													
Tyr	Thr	Gln	Ser	Thr	Leu	Leu	Gly	Tyr	Val	Met	Gly	Ala	Thr	Leu	Asp
210	215	220													
Leu	Val	Gly	Ala	Ser	Ser	Phe	Met	Trp	Arg	Gln	Gln	His	Val	Ala	Gly
225	230	235	240												
His	His	Ser	Phe	Thr	Asn	Ile	Asp	His	Tyr	Asp	Pro	Asp	Ile	Arg	Val
245	250	255													
Lys	Asp	Pro	Asp	Leu	Arg	Arg	Val	Thr	Ser	Gln	Gln	Pro	Arg	Arg	Trp
260	265	270													
Phe	His	Glu	Tyr	Gln	His	Ile	Tyr	Leu	Gly	Val	Leu	Tyr	Gly	Val	Leu
275	280	285													
Ala	Leu	Lys	Ser	Val	Leu	Ile	Asp	Asp	Phe	Ser	Ala	Phe	Phe	Ser	Gly
290	295	300													
Ala	Ile	Gly	Pro	Val	Lys	Ile	Ala	Gln	Met	Thr	Pro	Leu	Glu	Met	Gly
305	310	315	320												
Val	Phe	Trp	Gly	Gly	Lys	Val	Val	Tyr	Ala	Leu	Tyr	Met	Phe	Leu	Leu
325	330	335													
Pro	Met	Met	Tyr	Gly	Gln	Tyr	Asn	Ile	Leu	Thr	Phe	Ile	Gly	Leu	Tyr
340	345	350													
Ile	Leu	Ser	Gln	Leu	Val	Ala	Gly	Trp	Thr	Leu	Ala	Leu	Phe	Phe	Gln
355	360	365													
Val	Ala	His	Val	Val	Asp	Asp	Ala	Val	Phe	Pro	Val	Ala	Glu	Thr	Asp
370	375	380													
Gly	Gly	Lys	Ala	Lys	Ile	Pro	Ser	Gly	Trp	Ala	Glu	Met	Gln	Val	Arg
385	390	395	400												
Thr	Thr	Thr	Asn	Phe	Ser	Ser	Arg	Ser	Met	Phe	Trp	Thr	His	Ile	Ser
405	410	415													
Gly	Gly	Leu	Asn	His	Gln	Ile	Glu	His	His	Leu	Phe	Pro	Gly	Val	Cys
420	425	430													
His	Val	His	Tyr	Pro	Ser	Ile	Gln	Pro	Ile	Val	Lys	Ala	Thr	Cys	Asp
435	440	445													
Glu	Phe	Asn	Val	Pro	Tyr	Thr	Ser	Tyr	Pro	Thr	Phe	Trp	Ala	Ala	Leu
450	455	460													
Arg	Ala	His	Phe	Gln	His	Leu	Lys	Asn	Val	Gly	Leu	Gln	Asp	Gly	Leu
465	470	475	480												
Arg	Leu	Asp	Gly												

<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<220>
<221> n
<222> (12)

<400> 7
tggtggaarg anaarcayaa 20

<210> 8
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<220>
<221> modified_base
<222> (4)
<223> i

<220>
<221> modified_base
<222> (7)
<223> i

<220>
<221> modified_base
<222> (10)
<223> i

<220>
<221> modified_base
<222> (13)
<223> i

<400> 8
rttnarnccn ccngtraacc a 21

<210> 9
<211> 22
<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 9

aagttgcctt cgatgttct gg

22

<210> 10

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 10

gctcgccctgg agcaaggaaa tc

22

<210> 11

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<220>

<221> modified_base

<222> (3)

<223> i

<220>

<221> modified_base

<222> (18)

<223> i

<400> 11

gtngarttya tggayacngt

20

<210> 12

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

(15)

<220>
<221> modified_base
<222> (3)
<223> i

<220>
<221> modified_base
<222> (12)
<223> i

<400> 12
cknccccara anarrraytt

20

<210> 13
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 13
gcgagcttcc tcgttcttcc cc

22

<210> 14
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 14
tatgatttg aagcgcaaca cg

22

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<220>
<221> modified_base
<222> (6)

(16)

<223> i

<220>
<221> modified_base
<222> (9)
<223> i

<220>
<221> modified_base
<222> (14)
<223> i

<400> 15
athrangrna arntaygay gt

22

<210> 16
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
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<220>
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<222> (3)
<223> i

<220>
<221> modified_base
<222> (6)
<223> i

<220>
<221> modified_base
<222> (9)
<223> i

<220>
<221> modified_base
<222> (18)
<223> i

<400> 16
ggnaynkwns sdatrcngg rtc

23

<210> 17
<211> 22

(17)

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 17
gtgtgtacga tccgtggtta cc 22

<210> 18
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 18
aaggcgggac aggattcaac ac 22

<210> 19
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 19
ggaattcgcg atggcctcgat ccaccaccac 30

<210> 20
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 20
ggaattctac ttgcgcagcg tatgctacc 29

<210> 21
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
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<400> 21
ggaattcgcg atggaggcgt acgagatgg 29

<210> 22
<211> 29
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<213> Artificial Sequence

<220>
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<400> 22
ggaattcttc tgcccttttg ctcttgatc 29

<210> 23
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
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<400> 23
gttgaattcg acagtttatgc cgccacacgc 30

<210> 24
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 24
gttgaattca ggcccaaagc atgctgtcac 30

<210> 25
<211> 28
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 25

cgggatcctc tcctggcgca ccatcgtc

28

<210> 26

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 26

gggttaccaa cgcgcttcc caccaacg

28

<210> 27

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 27

gctctagagc gatggcctcg tccaccacc

29

<210> 28

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 28

gctctagact atacttcgc agcgtatgc

29

<210> 29

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 29
gctctagac gatggaggcg tacgagatgg 30

<210> 30
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 30
gctctagatt attctgcctt tttgctc 27

<210> 31
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 31
gctctagaga cagttatgcc gccacacgc 29

<210> 32
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 32
gctctagaag gcccaaagca tgctgtcac 29

<210> 33
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Primer

<400> 33
caggaaacag ctatgacc 18
(21)

<210> 34

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 34

aaactgcaga ttcccgatct agtaacata

30

<210> 35

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 35

ccggaaattcg catgcctgca ggtccccaga

30

<210> 36

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Primer

<400> 36

tgtaaaacga cggccagt

18

<210> 37

<211> 7

<212> PRT

<213> Unknown Organism

<220>

<221> Xaa

<222> (4)

<223> Description of Unknown Organism:conserved amino acid sequence

<400> 37

Trp Trp Lys Xaa Lys His Asn
1 5

<210> 38
<211> 7
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism:conserved amino acid sequence

<400> 38
Trp Phe Thr Gly Gly Leu Asn
1 5

<210> 39
<211> 7
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism:conserved amino acid sequence

<400> 39
Val Glu Phe Met Asp Thr Val
1 5

<210> 40
<211> 7
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism:conserved amino acid sequence

<400> 40
Lys Tyr Leu Phe Trp Gly Arg
1 5

<210> 41
<211> 8
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism:conserved amino acid sequence

<220>
<221> Xaa
<222> (2)
<223> Glu or Asn

<220>
<221> Xaa
<222> (3)
<223> Gly or Asp

<400> 41
Ile Xaa Xaa Lys Val Tyr Asp Val
1 5

<210> 42
<211> 8
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism:conserved amino acid sequence

<220>
<221> Xaa
<222> (5)
<223> Gln or Asp

<220>
<221> Xaa
<222> (6)
<223> Tyr or Thr

<220>
<221> Xaa
<222> (7)
<223> Met or Val

<400> 42
Asp Pro Asp Ile Xaa Xaa Xaa Pro
1 5

<210> 43

<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer
XbaMpELOf

<400> 43
agtctctaga gcgatggagg cgtacg 26

<210> 44
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer
SacMpELOr

<400> 44
cagttagctc ggtgtcttat tctgcc 26

<210> 45
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer XbaMpD5f

<400> 45
agcttctaga gccatgccgc cacacgccc 29

<210> 46
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer SacMpD5r

<400> 46
cagttagctc tcagccatcc agtcgt 26